



## SEQUENCE LISTING

<110> COEN, LAURENT  
PINZOLAS, ROSARIO OSTA  
BRULET, PHILIPPE

<120> HYBRID PROTEINS THAT MIGRATE RETROGRADELY AND  
TRANSYNAPTICALLY INTO THE CNS

<130> 03495.0174-01000

<140> 09/816,467

<141> 2001-03-26

<150> 60/055,615

<151> 1997-08-14

<150> 60/065,236

<151> 1997-11-13

<160> 19

<170> PatentIn Ver. 2.1

<210> 1

<211> 1600

<212> DNA

<213> Clostridium tetani

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<221> CDS

<222> (88)..(1476)

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Met Val Phe Ser Thr Pro Ile Pro Phe  
1 5

tct tat tct aaa aat ctg gat tgt tgg gtt gat aat gaa gaa gat ata 162  
Ser Tyr Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile  
10 15 20 25

gat gtt ata tta aaa aag agt aca att tta aat tta gat att aat aat 210  
Asp Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn  
30 35 40

gat att ata tca gat ata tct ggg ttt aat tca tct gta ata aca tat 258  
Asp Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr  
45 50 55

cca gat gct caa ttg gtg ccc gga ata aat ggc aaa gca ata cat tta 306  
Pro Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu  
60 65 70

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gta aac aat gaa tct tct gaa gtt ata gtg cat aaa gct atg gat att	354
Val Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile	
75 80 85	
gaa tat aat gat atg ttt aat aat ttt acc gtt agc ttt tgg ttg agg	402
Glu Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg	
90 95 100 105	
gtt cct aaa gta tct gct agt cat tta gaa caa tat ggc aca aat gag	450
Val Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn Glu	
110 115 120	
tat tca ata att agc tct atg aaa aaa cat agt cta tca ata gga tct	498
Tyr Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser	
125 130 135	
ggg tgg agt gta tca ctt aaa ggt aat aac tta ata tgg act tta aaa	546
Gly Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys	
140 145 150	
gat tcc gcg gga gaa gtt aga caa ata act ttt agg gat tta cct gat	594
Asp Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp	
155 160 165	
aaa ttt aat gct tat tta gca aat aaa tgg gtt ttt ata act att act	642
Lys Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile Thr	
170 175 180 185	
aat gat aga tta tct tct gct aat ttg tat ata aat gga gta ctt atg	690
Asn Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu Met	
190 195 200	
gga agt gca gaa att act ggt tta gga gct att aga gag gat aat aat	738
Gly Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn Asn	
205 210 215	
ata aca tta aaa cta gat aga tgt aat aat aat aat caa tac gtt tct	786
Ile Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val Ser	
220 225 230	
att gat aaa ttt agg ata ttt tgc aaa gca tta aat cca aaa gag att	834
Ile Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu Ile	
235 240 245	
gaa aaa tta tac aca agt tat tta tct ata acc ttt tta aga gac ttc	882
Glu Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp Phe	
250 255 260 265	
tgg gga aac cct tta cga tat gat aca gaa tat tat tta ata cca gta	930
Trp Gly Asn Pro Leu Arg Tyr Asp Thr Glu Tyr Tyr Leu Ile Pro Val	
270 275 280	
gct tct agt tct aaa gat gtt caa ttg aaa aat ata aca gat tat atg	978
Ala Ser Ser Ser Lys Asp Val Gln Leu Lys Asn Ile Thr Asp Tyr Met	
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tat ttg aca aat gcg cca tcg tat act aac gga aaa ttg aat ata tat 1026  
 Tyr Leu Thr Asn Ala Pro Ser Tyr Thr Asn Gly Lys Leu Asn Ile Tyr  
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tat aga agg tta tat aat gga cta aaa ttt att ata aaa aga tat aca 1074  
 Tyr Arg Arg Leu Tyr Asn Gly Leu Lys Phe Ile Ile Lys Arg Tyr Thr  
 315 320 325

cct aat aat gaa ata gat tct ttt gtt aaa tca ggt gat ttt att aaa 1122  
 Pro Asn Asn Glu Ile Asp Ser Phe Val Lys Ser Gly Asp Phe Ile Lys  
 330 335 340 345

tta tat gta tca tat aac aat aat gag cac att gta ggt tat ccg aaa 1170  
 Leu Tyr Val Ser Tyr Asn Asn Asn Glu His Ile Val Gly Tyr Pro Lys  
 350 355 360

gat gga aat gcc ttt aat aat ctt gat aga att cta aga gta ggt tat 1218  
 Asp Gly Asn Ala Phe Asn Asn Leu Asp Arg Ile Leu Arg Val Gly Tyr  
 365 370 375

aat gcc cca ggt atc cct ctt tat aaa aaa atg gaa gca gta aaa ttg 1266  
 Asn Ala Pro Gly Ile Pro Leu Tyr Lys Lys Met Glu Ala Val Lys Leu  
 380 385 390

cgt gat tta aaa acc tat tct gta caa ctt aaa tta tat gat gat aaa 1314  
 Arg Asp Leu Lys Thr Tyr Ser Val Gln Leu Lys Leu Tyr Asp Asp Lys  
 395 400 405

aat gca tct tta gga cta gta ggt acc cat aat ggt caa ata ggc aac 1362  
 Asn Ala Ser Leu Gly Leu Val Gly Thr His Asn Gly Gln Ile Gly Asn  
 410 415 420 425

gat cca aat agg gat ata tta att gca agc aac tgg tac ttt aat cat 1410  
 Asp Pro Asn Arg Asp Ile Leu Ile Ala Ser Asn Trp Tyr Phe Asn His  
 430 435 440

tta aaa gat aaa att tta gga tgt gat tgg tac ttt gta cct aca gat 1458  
 Leu Lys Asp Lys Ile Leu Gly Cys Asp Trp Tyr Phe Val Pro Thr Asp  
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gag gga tgg aca aat gat taaacagatt gatattgttca tgacatatgc 1506  
 Glu Gly Trp Thr Asn Asp  
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 Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp Ile Ile Ser Asp Ile Ser  
 35 40 45  
 Gly Phe Asn Ser Ser Val Ile Thr Tyr Pro Asp Ala Gln Leu Val Pro  
 50 55 60  
 Gly Ile Asn Gly Lys Ala Ile His Leu Val Asn Asn Glu Ser Ser Glu  
 65 70 75 80  
 Val Ile Val His Lys Ala Met Asp Ile Glu Tyr Asn Asp Met Phe Asn  
 85 90 95  
 Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser  
 100 105 110  
 His Leu Glu Gln Tyr Gly Thr Asn Glu Tyr Ser Ile Ile Ser Ser Met  
 115 120 125  
 Lys Lys His Ser Leu Ser Ile Gly Ser Gly Trp Ser Val Ser Leu Lys  
 130 135 140  
 Gly Asn Asn Leu Ile Trp Thr Leu Lys Asp Ser Ala Gly Glu Val Arg  
 145 150 155 160  
 Gln Ile Thr Phe Arg Asp Leu Pro Asp Lys Phe Asn Ala Tyr Leu Ala  
 165 170 175  
 Asn Lys Trp Val Phe Ile Thr Ile Thr Asn Asp Arg Leu Ser Ser Ala  
 180 185 190  
 Asn Leu Tyr Ile Asn Gly Val Leu Met Gly Ser Ala Glu Ile Thr Gly  
 195 200 205  
 Leu Gly Ala Ile Arg Glu Asp Asn Asn Ile Thr Leu Lys Leu Asp Arg  
 210 215 220  
 Cys Asn Asn Asn Asn Gln Tyr Val Ser Ile Asp Lys Phe Arg Ile Phe  
 225 230 235 240  
 Cys Lys Ala Leu Asn Pro Lys Glu Ile Glu Lys Leu Tyr Thr Ser Tyr  
 245 250 255  
 Leu Ser Ile Thr Phe Leu Arg Asp Phe Trp Gly Asn Pro Leu Arg Tyr  
 260 265 270  
 Asp Thr Glu Tyr Tyr Leu Ile Pro Val Ala Ser Ser Ser Lys Asp Val  
 275 280 285  
 Gln Leu Lys Asn Ile Thr Asp Tyr Met Tyr Leu Thr Asn Ala Pro Ser  
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 Tyr Thr Asn Gly Lys Leu Asn Ile Tyr Tyr Arg Arg Leu Tyr Asn Gly  
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 340 345 350  
 Asn Glu His Ile Val Gly Tyr Pro Lys Asp Gly Asn Ala Phe Asn Asn  
 355 360 365  
 Leu Asp Arg Ile Leu Arg Val Gly Tyr Asn Ala Pro Gly Ile Pro Leu  
 370 375 380  
 Tyr Lys Lys Met Glu Ala Val Lys Leu Arg Asp Leu Lys Thr Tyr Ser  
 385 390 395 400  
 Val Gln Leu Lys Leu Tyr Asp Asp Lys Asn Ala Ser Leu Gly Leu Val  
 405 410 415  
 Gly Thr His Asn Gly Gln Ile Gly Asn Asp Pro Asn Arg Asp Ile Leu  
 420 425 430  
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<212> DNA

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 aatgatatta tatcagatat atctgggttt aattcatctg taataacata tccagatgct 180  
 caattgggtgc ccggaataaa tggcaaaagca atacatttag taaacaatga atcttctgaa 240  
 gttatagtgc ataaagctat ggatattgaa tataatgata tgtttaataa ttttaccgtt 300  
 agcttttggg tgaggggttc taaagtatct gctagtcatt tagaacaata tggcacaat 360  
 gagtattcaa taattagctc tatgaaaaaa catagtcctat caataggatc tggttggagt 420  
 gtatcactta aaggtaataa cttaatatgg actttaaaag attccgcggg agaagttaga 480  
 caaataactt ttagggattt acctgataaa tttaatgctt atttagcaaa taaatgggtt 540  
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 aaactagata gatgtaataa taataatcaa tacgtttcta ttgataaatt taggatattt 720  
 tgcaaagcat taaatccaaa agagattgaa aaattataca caagttattt atctataacc 780  
 tttttaagag acttctgggg aaaccttta cgatatgata cagaatatta tttaatacca 840  
 gtagcttcta gttctaaga tgttcaattg aaaaatataa cagattatat gtatttgaca 900  
 aatgcgccat cgtatactaa cggaaaattg aatatatatt atagaagggt atataatgga 960  
 ctaaaattta ttataaaaag atatacacct aataatgaaa tagattcttt tgttaaataca 1020  
 ggtgatttta ttaaattata tgtatcatat aacaataatg agcacattgt aggttatccg 1080  
 aaagatggaa atgcctttta taatcttgat agaattctaa gagtaggtta taatgcccc 1140  
 ggtatccctc tttataaaaa aatggaagca gtaaaattgc gtgattttaa aacctattct 1200  
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<210> 8
<211> 27
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<220>  
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 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
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 <210> 10  
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<210> 17  
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